

A Biochemical Pathway Tool for Visualization and Discovery Using Functional Genomics and Proteomics Data**Saraiya, P.^{1,2}, Duca, K.A.*¹, North, C.²****¹Virginia Bioinformatics Institute; ²Department of Computer Science, Virginia Polytechnic Institute and State University, Blacksburg, VA, USA**

The field of Human Computer Interaction (HCI) strongly focuses on the experience of end users and their needs as seen from their own perspective, *i.e.*, the context and specific tasks for which a tool is going to be employed. HCI professionals ensure that new software tools created to meet the needs of end users actually do meet those needs and are appropriately matched to users' backgrounds and, hence, are intuitive to use. Studies at Virginia Bioinformatics Institute have allowed us to conclude that there are several data visualization/analysis challenges associated with functional genomics and proteomics data streams that have yet to be met by current software. The most important challenge, in our estimation, is the ability to present results in a functionally significant way that leverages the domain expert's background knowledge.

Several interesting tools have been developed to address this problem. Several display microarray data within biochemical networks and metabolic pathways. While reporting a strong interest in such tools, many life scientists fail to make extensive use of them, as they require a significant amount of time investment to build the initial networks. Moreover, learning curves for using them effectively can be quite steep.

Our approach is to provide a network visualization software tool that can import or connect to pre-built biological networks from different sources, *e.g.*, local or remote databases and the research literature. With this capability, users can construct their own networks by composition and modification rather than starting from scratch with each pathway of interest. By permitting multiple pathways to be displayed simultaneously, users can more easily discover connectivity between pathways and quickly appreciate the impact of other pathways on the biochemical events of most relevance to them. We also believe a standardized biochemical network syntax is necessary and adopt the format used in the Signal Transduction and Knowledge Environment (STKE) connection maps. The software will be implemented in Java for platform independence. It will accept standard database formats for microarray experiments as input and be designed to allow direct loading of biochemical pathways implemented with tools such as GeneMapp, Knowledge Editor, and STKE.